

## FIGURE 84

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT  
CGCCATGGGACACCACCAGGTACAGCAAGTGGGCGGCGAGCTCCGAGGAGGTCCCCGAGGGC  
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCTCTGGTC  
ACCACAGTCTTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGAGCGCGC  
GGCGCTGCTTGGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGCGCTGG  
GTGCCCTGAAGGAGGAGGTGGGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG  
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT  
GCGGGAACTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGCGAGGGGCCGTGAGGACG  
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACTCCTGCGAGCCG  
TGCCCCACGTCTGTGGCTGTCTTCGAGGGCTCCTGTACTTTTTCTCTGTGCCAAAGACGAC  
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC  
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GCTGTGCGCCATCTGGGCAAGGTTGAGGGCTACCACTGGGTGGACGGAGTCTCTCTCAGCTT  
CAGCCACTGGAACACAGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTGATGATGC  
TGACACGCGGGCTGTGGAACGACGACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG  
AAAAGGCACAACTGCTGAGACCCCGCCAGTGCCCTGGAGCCGCGCCCATTGACAGCATGTCGTA  
TCCTGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTTCTTCTCT  
CATCCACCGTGTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCC  
TGGGCTCTGGGACCTCCATGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACTAACC  
TCCACTAGCTCCTAAATCCCTGCTCCTGCGTCCCGTGATATGCTCCACTTCTCTCCCTAA  
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACCTGGA  
AGCTGTTTTTGACGCTGAGGAAGCATCAATAAATATTTGAGAAATGAAAAA

## **FIGURE 85**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352  
<subunit 1 of 1, 293 aa, 1 stop  
<MW: 32562, pI: 6.53, NX(S/T): 2  
MDTTRYSKWGSSEVPGGPWGRWVHWSRRPLFLALAVLVTTLWAVILSILLSKASTERAA  
LLDGHDLRLTNASKQTAALGALKKEEVGDCHSCCSGTQAQLQTTRAEELGEAQAKLMEQESALR  
ELRERVTVQGLAEAGRGREDVRTELFRALEAVRLQNNSCPCPTSWLSFEGSCYFFSVPKTTW  
AAQDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGRAVRHLGKVQGYQWVDGVSLSFS  
HWNQGEPNDAWGRENVMMLHTGLWNDAPCDSEKDGWICEKRHNC

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 31-54

#### **N-glycosylation sites.**

amino acids 73-76 and 159-162

#### **Leucine zipper pattern.**

amino acids 102-123

#### **N-myristoylation sites.**

amino acids 18-23, 133-138 and 242-247

#### **C-type lectin domain signature.**

amino acids 264-287

10561 562760

**Figure 1**

CCACGGGGGAAGAGGGTGATCCGACCCGGGGAGGTCGCTGGGCAGGGCGAGTTGGGAAAAGCG  
GCAGCCCCCGCCGCCCGCAGCCCCCTTCTCCTCCTTTCTCCACGCTCTATCTGCCTCTCG  
CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAACCTGGAGCCTCATTGGCCGGCCCCGG  
GGCGCCGGCCTCGGGCTTAAATAGGAGCTCGGGCTCTGGCTGGGACCCGACCCTGCCCGC  
CGCGCTCCCGCTGCTCCTGCGGGGTGATGGAAAACCCGACCCGGCCGCGCGCCTTGGGCAG  
GCCCTCTGCGCTCTCCTCCTGGCCACTCTCGGCGCCGCCGGCCAGCCTCTTGGGGGAGAGTC  
CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTACCGGCAAGTGGAGCCAGA  
CGGCCTTCCCCAAGCAGTACCCCCGTGTTCCGCCCCCCCTGCGCAGTGGTCTTCGCTGCTGGGG  
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTGAGTAACGGGCTGCG  
CGACTTTGCGGAGCGCGGCGAGGCCCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGGGGAGG  
CGCTGCAGAGCGTGCACGAGGTGTTTTCGGCGCCCGCCGTCCCAGCGGCACCGGGCAGACG  
TCGGCGAGCTGGAGGTTCGCGCAGCGCAGCATCGCTGGTCTGTTTGTGTGCGCATCTGTCG  
CAGCCCCGACTGAGTTCTGTGGCGCTGGACAGCCCTGGACCTGTGCGACAGGGGACCGTTGCGGG  
AACAGGCGGCGCTGGAACTGTACCCCTACAGACGCCGGGACGGACAGCGGCTTCACTTCTTC  
TCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCCTCCTCTCCAG  
CCACCCGGCCAACTCCTTCTACTACCCGCGGCTGAAGGCCCTGCCTCCCATCGCCAGGGTGA  
CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCTGCCCCAGC  
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CCTGTGGTCTCCTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA  
CTCGTACGTCCGGGCTCAGCCCGCCAACAACGGGAGCCCCTGCCCCGAGCTCGAAGAAGAG  
GCTGAGTGCCTCCCTGATAACTGCGTCTTAAGACCAGAGCCCGCAGCCCCCTGGGGCCCCCG  
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GGTTTCGCGCTGCTCTCGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCCT  
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GTTGCTCACAAAAA